

P21250.A01

13. (Amended-Clean Text) The data record according to claim 12, wherein its identifier is generated by a method of determining a substantially unique identifier of an alignment information, wherein the identifier is determined using and depending on only and all of a data on a gap information and identifiers of sequences in a sequence information.

14. (Amended-Clean Text) A method of storing, searching and/or communicating method of an alignment information which employs at least the data record according to claim 12.

15. (Amended-Clean Text) The method according to claim 1 which employs the correspondence information instead of the gap information.

16. (Amended-Clean Text) The method according to claim 1 which employs eigen-identifier of sequences in the sequence information.

REMARKS

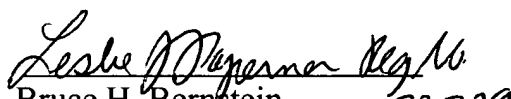
By the above amendment, the claims have been amended to delete multiple dependency.

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P21250.A01

If there should be any questions, the Examiner is invited to contact the undersigned
at the telephone number listed below.

Respectfully submitted,
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MARKED-UP COPY OF AMENDED CLAIMS

5. (Amended) The method according to claim 1 [any one of claims 1 to 4], in which the gap information is described by using the residue number and/or the number of residues which indicates the location and the length of a gap region existing in the alignment information of more than two sequences, or a numerical data convertible to those numbers by calculation.

6. (Amended) The method according to claim 1 [any one of claims 1 to 4], in which the gap information is described by using a data containing the residue number of another sequence not included in the alignment or a virtual sequence or column number of a standard representation of the alignment information or a numerical data convertible to the data.

7. (Amended) A method of generating a gap information of a new alignment information by calculating on only a gap information generated from an information of one or more alignments by any one of the methods according to claim 1 [claims 1 to 6].

8. (Amended) A method of obtaining a standard representation of an alignment information from both a gap information and a sequence information obtained by the method according to claim 1 [any one of claims 1 to 7].

09069312.110801

P21250.A01

12. (Amended) A data record including at least its identifier and a gap information and identifiers of sequences in a sequence information generated by the method according to claim 1 [any one of claims 1 to 10], and a media containing one or more of the record.

13. (Amended) The data record according to claim 12, wherein its identifier is generated by [the method according to claim 11] a method of determining a substantially unique identifier of an alignment information, wherein the identifier is determined using and depending on only and all of a data on a gap information and identifiers of sequences in a sequence information.

14. (Amended) A method of storing, searching and/or communicating method of an alignment information which employs at least the data record according to claim 12 [or claim 13].

15. (Amended) The method according to claim 1 [any one of claims 1 to 14] which employs the correspondence information instead of the gap information.

16. (Amended) The method according to claim 1 [any one of claims 1 to 15] which employs eigen-identifier of sequences in the sequence information.